

SEQUENCE LISTING

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<120> COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS
 OF HER-2/NEU-ASSOCIATED MALIGNANCIES

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<212> DNA

<213> Homo sapiens

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<211> 1773

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<213> Homo sapiens

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<211> 587

<212> PRT

<213> Homo sapiens

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Leu	Ala	Pro	Ser	Glu	Gly	Ala	Gly	Ser	Asp	Val	Phe	Asp	Gly	Asp	Leu	
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 Phe Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln Gly Gly
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 Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly Ala Pro Pro
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 <213> Homo sapiens

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 Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys Gly Ile
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 Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala Ile Lys Val
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 Ala Tyr Val Met Ala Gly Val Gly Ser Pro Tyr Val Ser Arg Leu Leu
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 Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Val Thr Gln Leu Met Pro
 115 120 125
 Tyr Gly Cys Leu Leu Asp His Val Arg Glu Asn Arg Gly Arg Leu Gly
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 Ser Gln Asp Leu Leu Asn Trp Cys Met Gln Ile Ala Lys Gly Met Ser
 145 150 155 160
 Tyr Leu Glu Asp Val Arg Leu Val His Arg Asp Leu Ala Ala Arg Asn
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 Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe Gly Leu
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 Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala Asp Gly Gly
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 Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu Arg Arg Arg
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 Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val Trp Glu
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35 40 45
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Phe Gly Thr Val Tyr Lys Gly Ile Trp Ile Pro Asp Gly Glu Asn Val
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 Lys Ile Pro Val Ala Ile Lys Val Leu Arg Glu Asn Thr Ser Pro Lys
 85 90 95
 Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Gly Val Gly
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 Ser Pro Tyr Val Ser Arg Leu Leu Gly Ile Cys Leu Thr Ser Thr Val
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 Gln Leu Val Thr Gln Leu Met Pro Tyr Gly Cys Leu Leu Asp His Val
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 Met Gln Ile Ala Lys Gly Met Ser Tyr Leu Glu Asp Val Arg Leu Val
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 Val Lys Ile Thr Asp Phe Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu
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 <212> PRT
 <213> Homo sapiens

<400> 11

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Gly	Ala	Met	Pro	Asn	Gln	Ala	Gln	Met	Arg	Ile	Leu	Lys	Glu	Thr	Glu		
	50					55					60						
Leu	Arg	Lys	Val	Lys	Val	Leu	Gly	Ser	Gly	Ala	Phe	Gly	Thr	Val	Tyr		
	65				70				75						80		
Lys	Gly	Ile	Trp	Ile	Pro	Asp	Gly	Glu	Asn	Val	Lys	Ile	Pro	Val	Ala		
				85					90					95			
Ile	Lys	Val	Leu	Arg	Glu	Asn	Thr	Ser	Pro	Lys	Ala	Asn	Lys	Glu	Ile		
		100						105					110				
Leu	Asp	Glu	Ala	Tyr	Val	Met	Ala	Gly	Val	Gly	Ser	Pro	Tyr	Val	Ser		
	115						120					125					
Arg	Leu	Leu	Gly	Ile	Cys	Leu	Thr	Ser	Thr	Val	Gln	Leu	Val	Thr	Gln		
	130					135					140						
Leu	Met	Pro	Tyr	Gly	Cys	Leu	Leu	Asp	His	Val	Arg	Glu	Asn	Arg	Gly		
	145				150				155						160		
Arg	Leu	Gly	Ser	Gln	Asp	Leu	Leu	Asn	Trp	Cys	Met	Gln	Ile	Ala	Lys		
				165					170					175			
Gly	Met	Ser	Tyr	Leu	Glu	Asp	Val	Arg	Leu	Val	His	Arg	Asp	Leu	Ala		
		180						185					190				
Ala	Arg	Asn	Val	Leu	Val	Lys	Ser	Pro	Asn	His	Val	Lys	Ile	Thr	Asp		
		195					200					205					
Phe	Gly	Leu	Ala	Arg	Leu	Leu	Asp	Ile	Asp	Glu	Thr	Glu	Tyr	His	Ala		
	210					215					220						
Asp	Gly	Gly	Lys	Val	Pro	Ile	Lys	Trp	Met	Ala	Leu	Glu	Ser	Ile	Leu		
	225				230					235					240		
Arg	Arg	Arg	Phe	Thr	His	Gln	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Val	Thr		
				245					250					255			
Val	Trp	Glu	Leu	Met	Thr	Phe	Gly	Ala	Lys	Pro	Tyr	Asp	Gly	Ile	Pro		
		260						265					270				
Ala	Arg	Glu	Ile	Pro	Asp	Leu	Leu	Glu	Lys	Gly	Glu	Arg	Leu	Pro	Gln		
		275					280					285					
Pro	Pro	Ile	Cys	Thr	Ile	Asp	Val	Tyr	Met	Ile	Met	Val	Lys	Cys	Trp		
		290				295					300						
Met	Ile	Asp	Ser	Glu	Cys	Arg	Pro	Arg	Phe	Arg	Glu	Leu	Val	Ser	Glu		
					310					315					320		

Phe Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln Asn
 325 330 335
 Glu Asp Leu Gly Pro Ala Ser Pro Leu Asp Ser Thr Phe Tyr Arg Ser
 340 345 350
 Leu Leu Glu Asp Asp Met Gly Asp Leu Val Asp Ala Glu Glu Tyr
 355 360 365
 Leu Val Pro Gln Gln Gly Phe Phe Cys Pro Asp Pro Ala Pro Gly Ala
 370 375 380
 Gly Gly Met Val His His Arg His Arg Ser Ser Ser Thr Arg Ser Gly
 385 390 395 400
 Gly Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu Glu Ala Pro
 405 410 415
 Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser Asp Val Phe Asp
 420 425 430
 Gly Asp Leu Gly Met Gly Ala Ala Lys Gly Leu Gln Ser Leu Pro Thr
 435 440 445
 His Asp Pro Ser Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr Val Pro
 450 455 460
 Leu Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu Thr Cys Ser Pro
 465 470 475 480
 Gln Pro Glu Tyr Val Asn Gln Pro Asp Val Arg Pro Gln Pro Pro Ser
 485 490 495
 Pro Arg Glu Gly Pro Leu Pro Ala Ala Arg Pro Ala Gly Ala Thr Leu
 500 505 510
 Glu Arg Pro Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp
 515 520 525
 Val Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro
 530 535 540
 Gln Gly Gly Ala Ala Pro Gln Pro His Pro Pro Ala Phe Ser Pro
 545 550 555 560
 Ala Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly
 565 570 575
 Ala Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn Pro Glu
 580 585 590
 Tyr Leu Gly Leu Asp Val Pro Val
 595 600

<210> 12
 <211> 957
 <212> DNA
 <213> Homo sapiens

<400> 12
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 gcccaagtga cccagaaccc aagatacctc atcacagtga ctggaagaa gttaacagt 120
 acttggtctc agaatatgaa ccatgagtat atgtcctggt atcgacaaga cccagggtg 180
 ggcttaaggc agatctacta ttcaatgaat gttgaggtga ctgataaggg agatgttct 240
 gaagggtaca aagtctctcg aaaagagaag aggaatttcc ccctgatcct ggagtcgcc 300
 agccccaacc agacctctct gtacttctgt gccagcagtt tagattgggg cgactagcg 360
 ggagggttgg gcacagatac gcagtatttt ggcccaggca cccggctgac agtgctcgag 420
 gacctgaaaa acgtgttccc acccgagggtc gctgtgtttg agccatcaga agcagagatc 480
 tcccacacct aaaaggccac actggtatgc ctggccacag gcttctaccc cgaccagtg 540
 gagctgagct ggtgggtgaa tgggaaggag gtgcacaagt ggggtcagca cagaccgca 600
 gccctcaag gagcaagccc gccctcaatg actccagata ctgctgagca gccgcctgag 660
 ggtctcggcc acttctggca gaacccccgc aaccacttcc gctgtcaagt ccagttctac 720
 gggctctcgg agaatgacga gtggacccag gatagggcc aacctgtcac ccagatcgtc 780

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agcgccgagg cctggggtag agcagactgt ggcttcacct ccgagtctta ccagcaaggg 840
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<210> 13
<211> 686
<212> DNA
<213> Homo sapiens

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aaatgcacct attcagtcctc tggaaaccct tatctttttt ggtatgttca atacccaac 180
cgaggcctcc agttccttct gaaatacatc acaggggata acctgggtta aggagctat 240
ggctttgaag ctgaatttaa caagagccaa acctccttcc acctgaagaa accatctgcc 300
cttgtagagc actccgcttt gtacttctgt gctgtgagac cgaattcagg atacagcacc 360
ctcacctttg ggaaggggac tatgcttcta gtctctccag atatccagaa ccctgaccct 420
gccgtgtacc agctgagaga ctctaaatcc agtgacaagt ctgtctgcct attcaccgat 480
tttgattctc aaacaaatgt gtcacaaagt aaggattctg atgtgtatat cacagacaaa 540
actgtgctag acatgaggtc tatggacttc aagagcaaca gtgctgtggc ctggagcaac 600
aaatctgact ttgcatgtgc aaacgccttc aacaacagca ttattccaga agacaccttc 660
ttccccagcc cagaaagttc ctgtga 686

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<210> 14
<211> 318
<212> PRT
<213> Homo sapiens

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      20      25      30
Val Thr Gly Lys Lys Leu Thr Val Thr Cys Ser Gln Asn Met Asn His
      35      40      45
Glu Tyr Met Ser Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Gln
      50      55      60
Ile Tyr Tyr Ser Met Asn Val Glu Val Thr Asp Lys Gly Asp Val Pro
      65      70      75      80
Glu Gly Tyr Lys Val Ser Arg Lys Glu Lys Arg Asn Phe Pro Leu Ile
      85      90      95
Leu Glu Ser Pro Ser Pro Asn Gln Thr Ser Leu Tyr Phe Cys Ala Ser
      100     105     110
Ser Leu Asp Trp Gly Gly Leu Ala Gly Gly Leu Gly Thr Asp Thr Gln
      115     120     125
Tyr Phe Gly Pro Gly Thr Arg Leu Thr Val Leu Glu Asp Leu Lys Asn
      130     135     140
Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile
      145     150     155     160
Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Tyr
      165     170     175
Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His
      180     185     190
Lys Trp Gly Gln His Arg Pro Ala Ala Pro Gln Gly Ala Ser Pro Pro
      195     200     205
Ser Met Thr Pro Asp Thr Ala Glu Gln Pro Pro Glu Gly Leu Gly His
      210     215     220

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Phe	Trp	Gln	Asn	Pro	Arg	Asn	His	Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr
225					230					235					240
Gly	Leu	Ser	Glu	Asn	Asp	Glu	Trp	Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val
				245					250						255
Thr	Gln	Ile	Val	Ser	Ala	Glu	Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe
			260					265					270		
Thr	Ser	Glu	Ser	Tyr	Gln	Gln	Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr
		275					280					285			
Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala
	290					295					300				
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<210> 15
 <211> 228
 <212> PRT
 <213> Homo sapiens

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				5					10					15	
Gly	Leu	Arg	Ala	Gln	Ser	Val	Ala	Gln	Pro	Glu	Asp	Gln	Val	Asn	Val
			20					25					30		
Ala	Glu	Gly	Asn	Pro	Leu	Thr	Val	Lys	Cys	Thr	Tyr	Ser	Val	Ser	Gly
		35					40					45			
Asn	Pro	Tyr	Leu	Phe	Trp	Tyr	Val	Gln	Tyr	Pro	Asn	Arg	Gly	Leu	Gln
	50					55					60				
Phe	Leu	Leu	Lys	Tyr	Ile	Thr	Gly	Asp	Asn	Leu	Val	Lys	Gly	Ser	Tyr
	65				70					75					80
Gly	Phe	Glu	Ala	Glu	Phe	Asn	Lys	Ser	Gln	Thr	Ser	Phe	His	Leu	Lys
			85						90					95	
Lys	Pro	Ser	Ala	Leu	Val	Ser	Asp	Ser	Ala	Leu	Tyr	Phe	Cys	Ala	Val
			100					105					110		
Arg	Pro	Asn	Ser	Gly	Tyr	Ser	Thr	Leu	Thr	Phe	Gly	Lys	Gly	Thr	Met
		115					120					125			
Leu	Leu	Val	Ser	Pro	Asp	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln
	130					135					140				
Leu	Arg	Asp	Ser	Lys	Ser	Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp
	145			150						155					160
Phe	Asp	Ser	Gln	Thr	Asn	Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr
			165					170						175	
Ile	Thr	Asp	Lys	Thr	Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser
		180					185						190		
Asn	Ser	Ala	Val	Ala	Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn
		195					200					205			
Ala	Phe	Asn	Asn	Ser	Ile	Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro
	210					215							220		
Glu	Ser	Ser	Cys												
225															

<210> 16
 <211> 48
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 <213> Artificial Sequence

<220>

<223> primer PDM-44

<400> 16

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48

<210> 17

<211> 45

<212> DNA

<213> Artificial Sequence

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<223> primer PDM-45

<400> 17

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45

<210> 18

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> primer PDM-591

<400> 18

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30

<210> 19

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> primer PDM-592

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<210> 20

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> primer PDM-72

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33

<210> 21

<211> 77

<212> DNA

<213> Artificial Sequence

<220>

<223> primer PDM-61

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 acgtccagac ccaggta 77

<210> 22
 <211> 37
 <212> DNA
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<220>
 <223> primer TCR Valpha-16 5'

<400> 22
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<210> 23
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer TCR alpha 3'

<400> 23
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<210> 24
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer TCR Vbeta-14. 5'

<400> 24
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<210> 25
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer TCR beta 3'

<400> 25
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